

Draft Genome Sequence of *Proteus mirabilis* NO-051/03, Representative of a Multidrug-Resistant Clone Spreading in Europe and Expressing the CMY-16 AmpC-Type β -Lactamase

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***Proteus mirabilis* NO-051/03, representative of a multidrug-resistant clone expressing the CMY-16 AmpC-type β -lactamase and circulating in Europe since 2003, was sequenced by a MiSeq platform using a paired-end approach. The genome was assembled in 100 scaffolds with a total length of 4,197,318 bp. Analysis of the draft genome sequence revealed the presence of several acquired resistance determinants to β -lactams, aminoglycosides, phenicols, tetracyclines, trimethoprim, and sulfonamides, of one plasmid replicon, and of a type I-E clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein (Cas) adaptive immune system.**

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Proteus mirabilis is one of the leading causes of urinary tract infections, especially in patients with functional or structural abnormalities of the urinary tract or with indwelling catheters, but it can also cause infections of other sites and bacteremia (1). In this species, which lacks functional chromosomal β -lactamase genes, acquired β -lactamase genes play an important role in the evolution of antibiotic resistance (2).

P. mirabilis NO-051/03 (also referred as IT NO-051/03) (3) was isolated in 2003 from a skin and soft tissue infection sample from a hospitalized patient from northern Italy (Novara) (4). The strain was resistant to penicillins and expanded-spectrum cephalosporins, due to the production of an acquired AmpC-type β -lactamase (ACBL) of the CMY lineage, named CMY-16 (3–5), and also to fluoroquinolones. The strain, which caused a clonal outbreak in northern Italy, was subsequently found to be highly related to a clone spreading in Europe and North Africa since the 1990s (3).

Bacterial DNA was subjected to whole-genome sequencing with a MiSeq platform (Illumina, Inc., San Diego, CA), using a 2 × 250-bp paired-end approach. In total, 2,216,404 reads were obtained and assembled using ABySS (6) into 100 scaffolds (>208 bp in size), with a total length of 4,197,318 bp and an N_{50} of 160,469 bp. The genome raw coverage was $\approx 130\times$. The average G+C content was 39%.

A total of 3,778 coding sequences (CDSs), 82 tRNAs, 48 rRNAs, and 2 clustered regularly interspaced short palindromic repeat (CRISPR) systems were annotated by PGAP (http://www.ncbi.nlm.nih.gov/genome/annotation_prok). Further analysis

showed the presence of a type I-E CRISPR-associated protein (Cas) adaptive immune system characterized by 20 spacers, of which 16 lacked any detectable identity with sequences in nucleotide databases, while 3 matched prophage sequences, and one matched a DNA fragment present between the *mucB* and *resD* genes in several conjugative IncL/M-type plasmids. These data suggest the ability of NO-051/03 to resist invasion by a number of phages and IncL/M-type plasmids.

The antimicrobial resistome of NO-051/03 was investigated with ResFinder (7), which confirmed the presence of two acquired β -lactamase genes (*bla*_{CMY-16} and *bla*_{TEM-1b}) and detected additional acquired resistance genes to aminoglycosides (*strAB*, *aacA4*, *aac(3)-I*, *aadA1*, and *aph(3')-Ic*), aminoglycosides and quinolones (*aac(6')Ib-cr*), chloramphenicol (*cat* and *catA1*), tetracyclines (*tet(A)*), trimethoprim (*dfrA1*), and sulfonamides (*sul1* and *sul2*). Further analysis of the quinolone resistance-determining regions of topoisomerase genes (8) showed the presence of mutations previously linked to reduced susceptibility to fluoroquinolones, namely, those encoding S83R in GyrA, S464Y in GyrB, and S80R in ParC.

PlasmidFinder (9) detected the presence of an IncQ1 replicon, while PHAST (10) revealed the presence of 5 intact, 2 incomplete, and 2 putative prophages.

To the best of our knowledge, this is the first genome sequencing project of a *P. mirabilis* isolate producing an ACBL. The results from this project are expected to broaden the knowledge on the genetic factors that have contributed to the successful international spread of such isolates.

Nucleotide sequence accession numbers. The complete genome sequence of *P. mirabilis* NO-051/03 was deposited at DDBJ/EMBL/GenBank databases under the accession number [LGAY00000000](https://www.ncbi.nlm.nih.gov/nuclseq/LGAY01000000). The version described in this paper is the first version, LGAY01000000.

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